NO:21). The probe set querying the changed base still has a perfect match (the G probe). However, probes in adjacent sets that overlap the altered target position (SEQ ID NOS:22-29) now have either one or two mismatches (red), instead of zero or one, since they were designed to match the target shown in panel A. (C) Hybridization to a 4L tiled array and detection of a base change in the target. The array shown was designed to the mt1 sequence. (Upper panel) hybridization to mt1. The substitution used in each row of probes is indicated to the left of the image. The target sequence can be read 5' to 3' from left to right as the complement of the substitution base with the brightest signal. With hybridization to mt2 (lower panel), which differs from mt1 in this region by a T →C transition, the G probe at position 16,493 is now a perfect match, with the other three probes having single base mismatches (A 5, C 3, G 37, T 4 counts). However, at flanking positions, the probes have either single or double base mismatches, since the mt2 transition now occurs away from the query position.

C1

Please enter the attached substitute sequence listing.

IN THE CLAIMS:

C2

1. (Three times amended) A segment of human mitochondrial DNA or RNA of between 10 and 100 bases including any one of the polymorphic sites shown in Table 1, wherein the polymorphic site within the segment is occupied by a base other than the base shown in Table 1, column 3 ("asn base") or the perfect complement of the full length of the segment.

C3

4. (Three times amended) An allele-specific oligonucleotide [that is perfectly complementary to a segment of human mitochondrial nucleic acid or its perfect complement including a polymorphic site shown in Table 1, column 1, wherein the polymorphic site within the segment is occupied by a base other than the base shown in Table 1, column 3 ("asn base")] comprising the segment or the full complement thereof as defined by claim 1.

C4

9. (Twice amended) An isolated nucleic acid comprising a segment of at least 10 contiguous bases from SEQ ID NO:30, or the perfect complement of the